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RAW SEQUENCE LISTING

DATE: 01/28/2002

PATENT APPLICATION: US/10/006,394

TIME: 11:32:53

Input Set : N:\Crif3\RULE60\10006394.raw

Output Set: N:\CRF3\01282002\J006394.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Yi Li and Mark D. Adams

7 (ii) TITLE OF INVENTION: Human G-Protein Receptor HIBEF51

9 (iii) NUMBER OF SEQUENCES: 10

11 (iv) CORRESPONDENCE ADDRESS:

13 (A) ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
14 Cecchi, Stewart & Olstein

15 (B) STREET: 6 Becker Farm Road

16 (C) CITY: Roseland

17 (D) STATE: NJ

18 (E) COUNTRY: US

19 (F) ZIP: 07068-1739

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk

23 (B) COMPUTER: IBM PC compatible

24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

25 (D) SOFTWARE: WordPerfect 5.1

27 (vi) CURRENT APPLICATION DATA:

C--> 28 (A) APPLICATION NUMBER: US/10/006,394

C--> 29 (B) FILING DATE: 10-Dec-2001

30 (C) CLASSIFICATION:

32 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: 09/228,420

34 (B) FILING DATE:

36 (viii) ATTORNEY/AGENT INFORMATION:

37 (A) NAME: MULLINS, J.G.

38 (B) REGISTRATION NUMBER: 33073

39 (C) REFERENCE/DOCKET NUMBER: 325800-453 (PF187)

41 (ix) TELECOMMUNICATION INFORMATION:

42 (A) TELEPHONE: 201-994-1700

43 (B) TELEFAX: 201-994-1744

46 (2) INFORMATION FOR SEQ ID NO: 1:

48 (i) SEQUENCE CHARACTERISTICS:

49 (A) LENGTH: 2764 base pairs

50 (B) TYPE: nucleic acid

51 (C) STRANDEDNESS: single

52 (D) TOPOLOGY: linear

54 (ii) MOLECULE TYPE: cDNA

57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

59 AATTACAGGT AACATTCTGA AATTGAACTA AACAGTAAAT TCTGTTGAAA TGTTTTCAAA 60

61 GAGGCAAAAT ATTATATTGG AATCAATGAA GAAAGTAAAT TATCTTGGCT AATTTTATTA 120

63 GTGGTAATTG TAGTGAAAGG TTTTCCTAAA TATTATAAGC AAATTCCTTT TCTCCCCCGT 180

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65 CTCAAATGAA AGGAAATGGG GGTAATTAAT TCTGACTGTG ATTGGTTTGT TTTTATGCTG 240
67 ATCTTGAAAG CTTGATGTTG CTGCTGCTCC TCATACAGTA CAGATCAGTT GTGTGGGGTG 300
69 CTATTGAGGG TAGCCGTGAA TAGTGGTGCC AGTAGGGGTG GAGCGGGAGG GATGATGCCA 360
71 GCCTGAGCTA GCCAGTTCTT TTGATTAGGG CATTGGATGT GAAATGTAAA ATGCTCTCTC 420
73 CTTTCTTCT ATCAGCTGTT CAGAGGAGAC TCATTACAAC TCCTGCTGAA GCTCCTAATC 480
75 TTCTTCCCTT CTCTTCTACC CTTTCCCCCT ACCCTCACTT GGCTGAAGA CGTTCTCCCC 540
77 AGAGTTTACC TTGCTCCCCT GGTGCTATGT GTATGGTGAA CCTGGCACTA TGGCCGCGTC 600
79 TGGGACTGGC CAGACAACCTG CTGCTGGCTC TCCTTATTCC AGGAAGGATT TAAAGGGGAA 660
81 TTGCACTGCA GGCAATGCAC CAGAGCAGCA GCATCAGGAG CTTGGGGAGT AAGGCTCCTC 720
83 TGGCATTATT ACACACATGC AAAGCTGACC GCAATGACAG CAGCTGCTTC TTTGAACTGT 780
85 TGGCAGCAGC CAAGCGGCAG CATGAAGTGA CAGATCACTC CTGAGCTCAA G ATG AAC 837
86 Met Asn
88 TCC ACC TTG GAT GGT AAT CAG AGC AGC CAC CCT TTT TGC CTC TTG GCA 885
89 Ser Thr Leu Asp Gly Asn Gln Ser Ser His Pro Phe Cys Leu Leu Ala
90 5 10 15
92 TTT GGC TAT TTG GAA ACT GTC AAT TTT TGC CTT TTG GAA GTA TTG ATT 933
93 Phe Gly Tyr Leu Glu Thr Val Asn Phe Cys Leu Leu Glu Val Leu Ile
94 20 25 30
96 ATT GTC TTT CTA ACT GTA TTG ATT ATT TCT GGC AAC ATC ATT GTG ATT 981
97 Ile Val Phe Leu Thr Val Leu Ile Ile Ser Gly Asn Ile Ile Val Ile
98 35 40 45 50
100 TTT GTA TTT CAC TGT GCA CCT TTG TTG AAC CAT CAC ACT ACA AGT TAT 1029
101 Phe Val Phe His Cys Ala Pro Leu Leu Asn His His Thr Thr Ser Tyr
102 55 60 65
104 TTT ATC CAG ACT ATG GCA TAT GCT GAC CTT TTT GTT GGG GTG AGC TGC 1077
105 Phe Ile Gln Thr Met Ala Tyr Ala Asp Leu Phe Val Gly Val Ser Cys
106 70 75 80
108 GTG GTC CCT TCT TTA TCA CTC CTC CAT CAC CCC CTT CCA GTA GAG GAG 1125
109 Val Val Pro Ser Leu Ser Leu Leu His His Pro Leu Pro Val Glu Glu
110 85 90 95
112 TCC TTG ACT TGC CAG ATA TTT GGT TTT GTA GTA TCA GTT CTG AAG AGC 1173
113 Ser Leu Thr Cys Gln Ile Phe Gly Phe Val Val Ser Val Leu Lys Ser
114 100 105 110
116 GTC TCC ATG GCT TCT CTG GCC TGT ATC AGC ATT GAT AGA TAC ATT GCC 1221
117 Val Ser Met Ala Ser Leu Ala Cys Ile Ser Ile Asp Arg Tyr Ile Ala
118 115 120 125 130
120 ATT ACT AAA CCT TTA ACC TAT AAT ACT CTG GTT ACA CCC TGG AGA CTA 1269
121 Ile Thr Lys Pro Leu Thr Tyr Asn Thr Leu Val Thr Pro Trp Arg Leu
122 135 140 145
124 CGC CTG TGT ATT TTC CTG ATT TGG CTA TAC TCG ACC CTG GTC TTC CTG 1317
125 Arg Leu Cys Ile Phe Leu Ile Trp Leu Tyr Ser Thr Leu Val Phe Leu
126 150 155 160
128 CCT TCC TTT TTC CAC TGG GGC AAA CCT GGA TAT CAT GGA GAT GTG TTT 1365
129 Pro Ser Phe Phe His Trp Gly Lys Pro Gly Tyr His Gly Asp Val Phe
130 165 170 175
132 CAG TGG TGT GCG GAG TCC TGG CAC ACC GAC TCC TAC TTC ACC CTG TTC 1413
133 Gln Trp Cys Ala Glu Ser Trp His Thr Asp Ser Tyr Phe Thr Leu Phe
134 180 185 190
136 ATC GTG ATG ATG TTA TAT GCC CCA GCA GCC CTT ATT GTC TGC TTC ACC 1461

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137 Ile Val Met Met Leu Tyr Ala Pro Ala Ala Leu Ile Val Cys Phe Thr
138 195                200                205                210
140 TAT TTC AAC ATC TTC CGC ATC TGC CAA CAG CAC ACA AAG GAT ATC AGC      1509
141 Tyr Phe Asn Ile Phe Arg Ile Cys Gln Gln His Thr Lys Asp Ile Ser
142                215                220                225
144 GAA AGG CAA GCC CGC TTC AGC AGC CAG AGT GGG GAG ACT GGG GAA GTG      1557
145 Glu Arg Gln Ala Arg Phe Ser Ser Gln Ser Gly Glu Thr Gly Glu Val
146                230                235                240
148 CAG GCC TGT CCT GAT AAG CGC TAT GCC ATG GTC CTG TTT CGA ATC ACT      1605
149 Gln Ala Cys Pro Asp Lys Arg Tyr Ala Met Val Leu Phe Arg Ile Thr
150                245                250                255
152 AGT GTA TTT TAC ATC CTC TGG TTG CCA TAT ATC ATC TAC TTC TTG TTG      1653
153 Ser Val Phe Tyr Ile Leu Trp Leu Pro Tyr Ile Ile Tyr Phe Leu Leu
154                260                265                270
156 GAA AGC TCC ACT GGC CAC AGC AAC CGC TTC GCA TCC TTC TTG ACC ACC      1701
157 Glu Ser Ser Thr Gly His Ser Asn Arg Phe Ala Ser Phe Leu Thr Thr
158 275                280                285                290
160 TGG CTT GCT ATT AGT AAC AGT TTC TGC AAC TGT GTA ATT TAT AGT CTC      1749
161 Trp Leu Ala Ile Ser Asn Ser Phe Cys Asn Cys Val Ile Tyr Ser Leu
162                295                300                305
164 TCC AAC AGT GTA TTC CAA AGA GGA CTA AAG CGC CTC TCA GGG GCT ATG      1797
165 Ser Asn Ser Val Phe Gln Arg Gly Leu Lys Arg Leu Ser Gly Ala Met
166                310                315                320
168 TGT ACT TCT TGT GCA AGT CAG ACT ACA GCC AAC GAC CCT TAC ACA GTT      1845
169 Cys Thr Ser Cys Ala Ser Gln Thr Thr Ala Asn Asp Pro Tyr Thr Val
170                325                330                335
172 AGA AGC AAA GGC CCT CTT AAT GGA TGT CAT ATC TGAAGTGGCT CAGTTACGGG      1898
173 Arg Ser Lys Gly Pro Leu Asn Gly Cys His Ile
174                340                345
176 GTTCCCGTGT GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT ATTTTATCTC TAAGTATTCC      1958
178 TAATTCACCTA GGAAATCTGG GACAGAATAC TTTGACTCTA AACAATAGCA TACAAATTAT      2018
180 TCGTATGGAT ACCTTCTAAG TTTGTAGAAA TGGTTTCCCG AAGTGCTTGT GAATTAGAAG      2078
182 ACTCAAGATC ATGAAGACAA ATTGCTCTTG CTCTCAATTT TTGAAATGTC TTGGAAATGA      2138
184 CTACAGTTCT CAGATTTAAA ATGAATAAAG CCATATCTAA CACCTCTTTC CAGCTGGCAT      2198
186 GACTGAACCT GAGTGTGAAA AGCGTCAGCA TTTTAAAAAG TCATCACTTT CTGTCACTT      2258
188 TCTGGGCTCT TTCCAGCTAT TTGGGCGTCA TATGCAATTG ATTTCTTCTA ACGGAATAGT      2318
190 AAAATATAAA TGAAAAGGTT TTAGAAATTA CTTTTTATGT ATGCCAAAGC ATAACACAC      2378
192 TGCAAGTTTC AACACTGTCA TTTAGAAAGC CAAATGTTCT GTGTTTTATT CTCTTGAGAG      2438
194 AATTCTCAGT AGGGTGAATA ATGTGAACAC ATAAACATTA ATTTTAGAAT TTTACAGTGA      2498
196 ACCATGAAGC AAAAGTGCAA TCAAATTATA CAATTTATGA AAAACTGAGC TACTTTTTGT      2558
198 GCCATGCTTC ACAGAGATCT AAAGATATGT GTGCCGTAGAA GTAATCGTGT AGTACTTTTG      2618
200 CCCATGCCTT TGTGTTATGT CTATATTTAG AATATCTGAA TTGTTAGATT TCTCTTTTAC      2678
202 AGCAAAATGT GCTTAAGCTA AAAAGTAATT CAGGGAATTC GATATCAAGC TTATCGATAC      2738
204 CGTCGACCTC GAGGGGGGGC CCGGTA
208 (2) INFORMATION FOR SEQ ID NO: 2:
210 (i) SEQUENCE CHARACTERISTICS:
211 (A) LENGTH: 349 amino acids
212 (B) TYPE: amino acid
213 (D) TOPOLOGY: Linear

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215      (ii) MOLECULE TYPE: protein
217      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
219 Met Asn Ser Thr Leu Asp Gly Asn Gln Ser Ser His Pro Phe Cys Leu
220              5              10              15
221 Leu Ala Phe Gly Tyr Leu Glu Thr Val Asn Phe Cys Leu Leu Glu Val
222              20              25              30
223 Leu Ile Ile Val Phe Leu Thr Val Leu Ile Ile Ser Gly Asn Ile Ile
224              35              40              45
225 Val Ile Phe Val Phe His Cys Ala Pro Leu Leu Asn His His Thr Thr
226              50              55              60
227 Ser Tyr Phe Ile Gln Thr Met Ala Tyr Ala Asp Leu Phe Val Gly Val
228 65              70              75              80
229 Ser Cys Val Val Pro Ser Leu Ser Leu Leu His His Pro Leu Pro Val
230              85              90              95
231 Glu Glu Ser Leu Thr Cys Gln Ile Phe Gly Phe Val Val Ser Val Leu
232              100             105             110
233 Lys Ser Val Ser Met Ala Ser Leu Ala Cys Ile Ser Ile Asp Arg Tyr
234              115             120             125
235 Ile Ala Ile Thr Lys Pro Leu Thr Tyr Asn Thr Leu Val Thr Pro Trp
236              130             135             140
237 Arg Leu Arg Leu Cys Ile Phe Leu Ile Trp Leu Tyr Ser Thr Leu Val
238 145             150             155             160
239 Phe Leu Pro Ser Phe Phe His Trp Gly Lys Pro Gly Tyr His Gly Asp
240              165             170             175
241 Val Phe Gln Trp Cys Ala Glu Ser Trp His Thr Asp Ser Tyr Phe Thr
242              180             185             190
243 Leu Phe Ile Val Met Met Leu Tyr Ala Pro Ala Ala Leu Ile Val Cys
244              195             200             205
245 Phe Thr Tyr Phe Asn Ile Phe Arg Ile Cys Gln Gln His Thr Lys Asp
246              210             215             220
247 Ile Ser Glu Arg Gln Ala Arg Phe Ser Ser Gln Ser Gly Glu Thr Gly
248 225             230             235             240
249 Glu Val Gln Ala Cys Pro Asp Lys Arg Tyr Ala Met Val Leu Phe Arg
250              245             250             255
251 Ile Thr Ser Val Phe Tyr Ile Leu Trp Leu Pro Tyr Ile Ile Tyr Phe
252              260             265             270
253 Leu Leu Glu Ser Ser Thr Gly His Ser Asn Arg Phe Ala Ser Phe Leu
254              275             280             285
255 Thr Thr Trp Leu Ala Ile Ser Asn Ser Phe Cys Asn Cys Val Ile Tyr
256              290             295             300
257 Ser Leu Ser Asn Ser Val Phe Gln Arg Gly Leu Lys Arg Leu Ser Gly
258 305             310             315             320
259 Ala Met Cys Thr Ser Cys Ala Ser Gln Thr Thr Ala Asn Asp Pro Tyr
260              325             330             335
261 Thr Val Arg Ser Lys Gly Pro Leu Asn Gly Cys His Ile
262              340             345
266 (2) INFORMATION FOR SEQ ID NO: 3:
268      (i) SEQUENCE CHARACTERISTICS:
269          (A) LENGTH: 358 amino acids

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270          (B) TYPE: amino acid
271          (C) STRANDEDNESS: Not Relevant
W--> 272          (D) TOPOLOGY: Not Relevant
274          (ii) MOLECULE TYPE: protein
276          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
W--> 278 Met Asn Ser Thr Leu Xaa Asp Gly Asn Gln Ser Ser His Pro Phe Cys
279          5 10 15
280 Leu Leu Ala Phe Gly Tyr Leu Glu Thr Val Asn Phe Cys Leu Leu Glu
281          20 25 30
W--> 282 Val Leu Ile Ile Val Xaa Xaa Xaa Xaa Phe Leu Thr Val Leu Ile Ile
283          35 40 45
284 Ser Gly Asn Ile Ile Val Ile Phe Val Phe His Cys Ala Pro Leu Leu
285          50 55 60
286 Asn His His Thr Thr Ser Tyr Phe Ile Gln Thr Met Ala Tyr Ala Asp
287          65 70 75 80
288 Leu Phe Val Gly Val Ser Cys Val Val Pro Ser Leu Ser Leu Leu His
289          85 90 95
W--> 290 His Pro Leu Pro Xaa Xaa Val Glu Glu Ser Leu Thr Cys Gln Ile Phe
291          100 105 110
292 Gly Phe Val Val Ser Val Leu Lys Ser Val Ser Met Ala Ser Leu Ala
293          115 120 125
294 Cys Ile Ser Ile Asp Arg Tyr Ile Ala Ile Thr Lys Pro Leu Thr Tyr
295          130 135 140
296 Asn Thr Leu Val Thr Pro Trp Arg Leu Arg Leu Cys Ile Phe Leu Ile
297          145 150 155 160
298 Trp Leu Tyr Ser Thr Leu Val Phe Leu Pro Ser Phe Phe His Trp Gly
299          165 170 175
300 Lys Pro Gly Tyr His Gly Asp Val Phe Gln Trp Cys Ala Glu Ser Trp
301          180 185 190
W--> 302 Xaa Xaa Xaa His Thr Asp Ser Tyr Phe Thr Leu Phe Ile Val Met Met
303          195 200 205
304 Leu Tyr Ala Pro Ala Ala Leu Ile Val Cys Phe Thr Tyr Phe Asn Ile
305          210 215 220
W--> 306 Phe Arg Ile Cys Gln Gln His Thr Lys Asp Ile Ser Glu Arg Xaa Xaa
307          225 230 235 240
W--> 308 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Ala Arg Phe Ser
309          245 250 255
W--> 310 Ser Gln Ser Gly Xaa Xaa Xaa Xaa Glu Thr Gly Glu Val Gln Ala Cys
311          260 265 270
312 Pro Asp Lys Arg Tyr Ala Met Val Leu Phe Arg Ile Thr Ser Val Phe
313          275 280 285
314 Tyr Ile Leu Trp Leu Pro Tyr Ile Ile Tyr Phe Leu Leu Glu Ser Ser
315          290 295 300
316 Thr Gly His Ser Asn Arg Phe Ala Ser Phe Leu Thr Thr Trp Leu Ala
317          305 310 315 320
318 Ile Ser Asn Ser Phe Cys Asn Cys Val Ile Tyr Ser Leu Ser Asn Ser
319          325 330 335
320 Val Phe Gln Arg Gly Leu Lys Arg Leu Ser Gly Ala Met Cys Thr Ser
321          340 345 350

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VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10006394.raw

Output Set: N:\CRF3\01282002\J006394.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:272 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=3
L:278 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:282 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:290 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:302 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:306 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:308 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:310 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:333 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=4
L:347 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:349 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:361 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:382 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4